

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 1999, 18:00:23 ; Search time 10.28 Seconds
(without alignments)
921.194 Million cell updates/sec

Title: US-09-126-945-2
Perfect score: 335
Sequence: 1 MGSASPGLSVSPSHLLLP.....GIIRKPDISQRLVYQFVHP1 335

Scoring table: OLIGO

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	7.2	114	1	ETS4_DROME
2	14	4.2	510	1	ERM_HUMAN
3	14	4.2	477	1	ETV1_MOUSE
4	14	4.2	477	1	ETV1_MOUSE
5	14	4.2	551	1	ETV4_MOUSE
6	14	4.2	555	1	ETV4_MOUSE
7	10	3.0	431	1	SAPA_HUMAN
8	10	3.0	430	1	SAPA_MOUSE
9	10	3.0	405	1	SAPA_MOUSE
10	8	2.4	247	1	DEVB_MYCLE
11	8	2.4	428	1	ELK1_HUMAN
12	8	2.4	429	1	ELK1_MOUSE
13	8	2.4	407	1	ELK3_HUMAN
14	8	2.4	409	1	ELK3_MOUSE
15	8	2.4	548	1	ERM_HUMAN
16	8	2.4	551	1	ERM_MOUSE
17	8	2.4	478	1	ERG_CHICK
18	8	2.4	462	1	ERG_HUMAN
19	8	2.4	173	1	ERG_LYTV
20	8	2.4	272	1	ERG_MOUSE
21	8	2.4	64	1	ETS3_DROME
22	8	2.4	102	1	ETS6_DROME
23	8	2.4	250	1	ETV3_HUMAN
24	8	2.4	452	1	FLI1_HUMAN
25	8	2.4	452	1	FLI1_MOUSE
26	8	2.4	453	1	FLI1_XENLA
27	7	2.1	421	1	ACDM_HUMAN
28	7	2.1	421	1	ACDM_MOUSE
29	7	2.1	421	1	ACDM_MOUSE
30	7	2.1	421	1	ACDM_PIG
31	7	2.1	444	1	CEFG_CEPAC
32	7	2.1	686	1	CNG1_HUMAN
33	7	2.1	333	1	DCTR_RHOCA
34	7	2.1	270	1	DNA_SRRMA
35	7	2.1	412	1	EGR2_BRARE
36	7	2.1	619	1	ELF1_HUMAN
37	7	2.1	619	1	ELF1_MOUSE
38	7	2.1	157	1	FKBP1_MOUSE
39	7	2.1	610	1	GLMS_THIFE
40	7	2.1	310	1	GTR1_YEAST
41	7	2.1	315	1	HAT3_ARATH
42	7	2.1	411	1	HON3_BRATL
43	7	2.1	311	1	LR4D_HUMAN

ALIGNMENTS

44 7 2.1 329 1 LB4D_PIG
45 7 2.1 692 1 YPH5_THIYI

Q29073 sus scrofa
P45365 thlocystis

RESULT	1	ETS4_DROME	STANDARD	PRT	114 AA.
ID	ETS4_DROME				
AC	P28775				
DT	01-APR-1993 (REL. 25, CREATED)				
DT	01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)				
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)				
DE	DNA-BINDING PROTEIN D-ETS-4 (FRAGMENT).				
DE	ETS98B OR ETS-4.				
OS	DROSOPHILA MELANOGASTER (FRUIT FLY).				
OC	EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;				
OC	PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;				
OC	DROSOPHILIDAE; DROSOPHILA.				
OC	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 922496640.				
RA	CHEN T., BUNTING W., KARIM F.D., THUMMEL C.S.:				
RT	"Isolation and characterization of five drosophila genes that encode				
RT	an ets-related DNA binding domain."				
RL	DEV. BIOL. 151:176-191(1992).				
CC	-1- SUBCELLULAR LOCATION: NUCLEAR.				
CC	-1- SIMILARITY: BELONGS TO THE ETS FAMILY.				
CC	-----				
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CC	-----				
DR	EMBL; M88474; G157196; ..				
DR	PIR; S28821; S28821.				
DR	FLYBASE; FBgn0005659; Ets98B.				
DR	PROSITE; PS00345; ETS_DOMAIN_1; 1.				
DR	PROSITE; PS00346; ETS_DOMAIN_2; 1.				
DR	PROSITE; PS50061; ETS_DOMAIN_3; 1.				
DR	PFAM; PF00178; Ets; 1.				
DR	HSP; O01543; IFL1.				
KW	DNA-BINDING; NUCLEAR PROTEIN.				
FT	NON_TER	1			
FT	DNA_BIND	26	108		ETS-DOMAIN.
FT	NON_TER	114	114		
SO	SEQUENCE	114 AA;	13051 MW;	E9003913 CRC32;	
Query Match		7.2%;	Score 24;	DB 1;	Length 114;
Best Local Similarity		100.0%;	Pred. No. 2e-17;		
Matches	24;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
OY	294 RKNRPAMNYDKLSRSIROYYKGI 317				
	71 RKNRPAMNYDKLSRSIROYYKGI 94				
RESULT	2				
ERM_HUMAN					
ID	ERM_HUMAN	STANDARD	PRT	510 AA.	
AC	P41161				
DT	01-FEB-1995 (REL. 31, CREATED)				
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)				
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)				
DE	ETS-RELATED PROTEIN ERM (ETS TRANSLLOCATION VARIANT 5).				
DE	ETV5 OR ERM.				
CN	HOMO SAPIENS (HUMAN).				
OC	EUMETAZOA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				

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OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE: 94203669.
RA MONTE D., BAERT J.-L., DEFOSSEZ P.-A., DE LAUNOIT Y., STEHELIN D.;
RT "Molecular cloning and characterization of human ERM, a new member of
RT the Ets family closely related to mouse PEA3 and ERM1 transcription
RT factors."
RL ONCOGENE 9:1397-1406(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE: 96297763.
RA MONTE D., COUTTE L., DEMITTE F., DEFOSSEZ P.-A., LE CONIAT D.,
RA STEHELIN R., BERGER Y., DE LAUNOIT Y.;
RT "Genomic organization of the human ERM (ETV5) gene, a PEA3 group
RT member of Ets transcription factors."
RL GENOMICS 35:236-240(1996).
CC -1- FUNCTION: BINDS TO DNA SEQUENCES CONTAINING THE CONSENSUS
CC NUCLEOTIDE CORE SEQUENCE GGAA.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: X76184; G479167; -
DR EMBL: X96381; E225719; -
DR EMBL: X96380; E225719; JOINED.
DR EMBL: X96382; E225719; JOINED.
DR EMBL: X96379; E225719; JOINED.
DR EMBL: X96378; E225719; JOINED.
DR EMBL: X96377; E225719; JOINED.
DR EMBL: X96376; E225719; JOINED.
DR EMBL: X96375; E225719; JOINED.
DR PIR: S43692; S43692.
DR MIM: 601600; -
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS00061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
DR DNA-BINDING; NUCLEAR PROTEIN.
RW DNA_BIND 368 448 ETS-DOMAIN.
FT SEQUENCE 510 AA; 57838 MW; 7581228D CRC32;
SQ

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Query Match 4.28; Score 14; DB 1; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 295 KNRPMANYDKLSRS 308
Db 412 KNRPMANYDKLSRS 425

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RESULT 3
ETV1_HUMAN STANDARD; PRT; 477 AA.
AC P50549;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ETS TRANSCRIPTION VARIANT 1 (ERM1 PROTEIN).
GN ETV1 OR ERM1.
OS HOMO SAPIENS (HUMAN).
OC CHORDATA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

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OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE: 95215084.
RA DEJON I.-S., DAVIS J.N., BRAUN B.S., SUBLETT J.E., ROUSSEL M.F.,
RA DENNY C.T., SHAPIRO D.N.;
RT "A variant Ewing's sarcoma translocation (7;22) fuses the EWS gene to
RT the Ets gene ETV1."
RL ONCOGENE 10:1229-1234(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE: 95380185.
RA MONTE D., COUTTE L., BAERT J.-L., ANGELI I., STEHELIN D.,
RA DE LAUNOIT Y.;
RT "Molecular characterization of the ets-related human transcription
RT factor ERM1."
RL ONCOGENE 11:771-779(1995).
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
CC CONTAINING THE CONSENSUS PENTANUCLEOTIDE 5'-CGGA(AT)-3'.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -1- TISSUE SPECIFICITY: VERY HIGHLY EXPRESSED IN BRAIN, HIGHLY
CC EXPRESSED IN TESTIS, LUNG AND HEART, MODERATELY IN SPLEEN, SMALL
CC INTESTINE, PANCREAS AND COLON, WEAKLY IN LIVER, PROSTATE AND
CC THYMUS, VERY WEAKLY IN SKELETAL MUSCLE, KIDNEY AND OVARY AND NOT
CC IN PLACENTA AND PERIPHERAL BLOOD LEUCOCYTES.
CC -1- DISEASE: A FORM OF EWING'S SARCOMA IS CHARACTERIZED BY A
CC CHROMOSOMAL TRANSLOCATION T(7;22)(P22;Q12) WHICH INVOLVES ETV1
CC AND EWS.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: U17163; G596006; -
DR EMBL: X87175; G1045061; -
DR MIM: 600541; -
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS00061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
RW TRANSCRIPTION REGULATION; ACTIVATOR; NUCLEAR PROTEIN; DNA-BINDING;
KW PROTO-ONCOGENE; CHROMOSOMAL TRANSLOCATION.
FT DNA_BIND 335 415 ETS-DOMAIN.
FT CONFLICT 39 39 L -> V (IN REF. 2).
FT CONFLICT 61 79 AOVNDQGVPPDQESL -> V (IN REF. 2).
FT FT 117 117 S -> C (IN REF. 2).
FT CONFLICT 127 127 N -> K (IN REF. 2).
FT CONFLICT 253 253 MISSING (IN REF. 2).
FT CONFLICT 349 349 S -> A (IN REF. 2).
SQ SEQUENCE 477 AA; 55100 MW; 75BD7133 CRC32;

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Query Match 4.28; Score 14; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 295 KNRPMANYDKLSRS 308
Db 379 KNRPMANYDKLSRS 392

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RESULT 4
ETV1_MOUSE STANDARD; PRT; 477 AA.
AC P41164;
DT 01-FEB-1995 (REL. 31, CREATED)

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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ERB1 PROTEIN (ETS TRANSLOCATION VARIANT 1).
ETV1 OR ETSRBP1 OR ERB1.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIURONATHI; MURIDAE; MURINAE; MUS.
[1]
SEQUENCE FROM N.A.
TISSUE-EMBRYO.
RX MEDLINE: 94040714.
RA BROWN T.A., MCKNIGHT S.L.;
"Specificities of protein-protein and protein-DNA interaction of GABP
alpha and two newly defined ets-related proteins."
RL GENES DEV. 6:2502-2512(1992).
-1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
CONTAINING THE CONSENSUS PENTANUCLEOTIDE 5'-CGGAAAT]-3'.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- TISSUE SPECIFICITY: ABUNDANT IN KIDNEY. MODERATE LEVELS SEEN IN
THE HEART, BRAIN, LUNG, EMBRYO AND LOWER LEVELS SEEN IN SPLEEN,
INTESTINE, TESTIS AND THYMUS.
-1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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DR EMBL: L10426; G515964; .
DR PIR: B46396; B46396.
DR MGI: 99254; ETSRBP1.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSSP: P14921; 25TW.
DR TRANSCRIPTION REGULATION; NUCLEAR PROTEIN; DNA-BINDING.
KM DNA_BIND 335 415 ETS-DOMAIN.
FT SEQUENCE 477 AA; 55040 MW; 670ADC77 CRC32;
SQ
Query Match 4.2%; Score 14; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 295 KNRPMANTDKLSRS 308
DB 379 KNRPMANTDKLSRS 392
RESULT 5
ETV4_HUMAN STANDARD: PRT; 551 AA.
ID ETV4_HUMAN
AC P43368;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ADENOVIRUS E1A ENHANCER BINDING PROTEIN (E1A-F) (ETS TRANSLOCATION
VARIANT 4) (FRAGMENT).
GN ETV4 OR E1AF.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95293380.
RA FRIDMAN L.S., OSTERMEYER E.A., LYNCH E.D., SZABO C.T., MEZA J.E.,
RA ANDERSON L.A., DOWD P., LEE M.K., ROWELL S.E., ELLISON J.,
RA BOYD J., KING M.C.;
RT "22 genes from chromosome 17q21: cloning, sequencing, and

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characterization of mutations in breast cancer families and tumors.";
GENOMICS 25:256-263(1995).
[2]
RN SEQUENCE OF 90-551 FROM N.A.
RP MEDLINE: 93181246.
RA HIRASHINO F., YOSHIDA K., FUJINAGA K., KAMIO K., FUJINAGA K.;
RT "Isolation of a cDNA encoding the adenovirus E1A enhancer binding
protein: a new human member of the ets oncogene family.";
RL NUCLEIC ACIDS RES. 21:547-553(1993).
-1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE ENHANCER OF
THE ADENOVIRUS E1A GENE; THE CORE-BINDING SEQUENCE IS
5' [ACGGAATG]-3'.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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DR EMBL: U18018; G602288; .
DR EMBL: D12765; G219611; .
DR MIM: 600711; .
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSSP: P14921; 25TW.
DR TRANSFAC: T00685; .
DR DNA_BINDING; NUCLEAR PROTEIN; ACTIVATOR; TRANSCRIPTION REGULATION.
KM DNA_BIND 1 1 ASP/GLU-RICH (ACIDIC).
FT NON_TER 1 1
FT DOMAIN 116 142 GLN-RICH.
FT DOMAIN 215 311 ETS-DOMAIN.
FT DNA_BIND 408 488 ETS-DOMAIN.
FT CONFLICT 91 94 GNGS -> EMGD (IN REF. 2).
FT SEQUENCE 551 AA; 60570 MW; 1F8D5E40 CRC32;
SQ
Query Match 4.2%; Score 14; DB 1; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 295 KNRPMANTDKLSRS 308
DB 452 KNRPMANTDKLSRS 465
RESULT 6
ETV4_MOUSE STANDARD: PRT; 555 AA.
ID ETV4_MOUSE
AC P28322;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE POLYOMAVIRUS ENHANCER ACTIVATOR 3 (PEA3 PROTEIN) (ETS TRANSLOCATION
VARIANT 4).
GN ETV4 OR PEA3 OR PEA-3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIURONATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92192459.
RA XIN J.-H., COMIE A., LACHANCE P., HASSELL J.A.;
RT "Molecular cloning and characterization of PEA3, a new member of the
Ets oncogene family that is differentially expressed in mouse
embryonic cells.";
RL GENES DEV. 6:481-496(1992).
-1- FUNCTION: BINDS TO THE PEA3 MOTIF (5'-AGGAG-3'). MAY PLAY A
REGULATORY ROLE DURING EMBRYOGENESIS.

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CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: EPIDIDYMIS AND THE BRAIN.
CC -1- PFM: PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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CC -----
DR EMBL: X63190; G53628;
DR PIR: S24061; S24061.
DR MGD: MGI:99423; PEK3.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PFM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
DR TRANSFAC: T00684;
DR DNA-BINDING: NUCLEAR PROTEIN; ACTIVATOR; TRANSCRIPTION REGULATION;
DR PHOSPHORYLATION.
KW DOMAIN 124 150 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 217 315 GLN-RICH.
FT DNA_BIND 412 492 ETS-DOMAIN.
SQ SEQUENCE 555 AA; 60846 MW; 084F57CE CRC32;

Query Match
Best Local Similarity 4.2%; Score 14; DB 1; Length 555;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNPANMYDKLSRS 308
DB 456 KNPANMYDKLSRS 469
|||||
RESULT 7
SAPA_HUMAN STANDARD; PRT; 431 AA.
AC P28324;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (SAP-1A) (ETS-DOMAIN
DE PROTEIN ELK-4).
GN ELK4 OR SAP1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 92154673.
RT "Characterization of SAP-1, a protein recruited by serum response
RT factor to the c-fos serum response element."
RL CELL 76:411-411(1994).
-1- FUNCTION: FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR
-1- (SRF). REQUIRES DNA-BOUND SRF FOR TERNARY COMPLEX FORMATION AND
-1- MAKES EXTENSIVE DNA-CONTACTS TO THE 5' SIDE OF SRF, BUT DOES NOT
-1- BIND DNA AUTONOMOUSLY.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- ALTERNATIVE PRODUCTS: TWO FORMS OF SAP-1 ARE PRODUCED BY
-1- ALTERNATIVE SPLICING OF THE SAME GENE, THEY ONLY DIFFER IN THE

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CC C-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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CC -----
DR EMBL: M85165; G429186;
DR PIR: B42093; B42093.
DR MIM: 600246;
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PFM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
DR TRANSFAC: T00737;
DR DNA-BINDING: NUCLEAR PROTEIN; ALTERNATIVE SPLICING.
FT DNA_BIND 5 85 ETS-DOMAIN.
SQ SEQUENCE 431 AA; 46827 MW; 2960052A CRC32;

Query Match
Best Local Similarity 3.0%; Score 10; DB 1; Length 431;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 VARLMGIRKN 296
DB 41 VARLMGIRKN 50
|||||
RESULT 8
SAPA_MOUSE STANDARD; PRT; 430 AA.
AC P41158;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (SAP-1A) (ETS-DOMAIN
DE PROTEIN ELK-4).
GN ELK4 OR SAP1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-EMBRYO;
RX MEDLINE: 95047310.
RA GIOVANE A.; PINTAS A.; MATRA S.-M.; SOBIESZCZUK P.; WASYLK B.;
RT "Net, a new eukaryotic transcription factor that is activated by Ras."
RT GENES DEV. 8:1502-1513(1994).
-1- FUNCTION: CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
-1- FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
-1- ELEMENT.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- TISSUE SPECIFICITY: LUNG AND LIVER.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: Z36885; G535128;
DR MGD: MGI:102853; ELK4.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.

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DR PROSITE: PSS0061; ETS_DOMAIN_3; 1.
 DR PRAM: PF00178; Ets; 1.
 DR HSSP: P14921; 25TW.
 KW DNA-BINDING: NUCLEAR PROTEIN.
 FT DNA_BIND 5 85 ETS-DOMAIN.
 SQ SEQUENCE 430 AA; 46867 MW; BE175C95 CRC32;

Query Match 3.0%; Score 10; DB 1; Length 430;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 VARLWGIRKN 296
 DB 41 VARLWGIRKN 50

RESULT 9
 SARP_HUMAN STANDARD; PRT; 405 AA.
 AC P28323;
 DT 01-DEC-1992 (REL. 24, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1B (SAP-1B) (ETS-DOMAIN
 DE PROTEIN ELK-4).
 GN ELK4 OR SAP1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92354673.
 RA DALTON S., TREISMAN R.;
 RT "Characterization of SAP-1, a protein recruited by serum response
 factor to the c-fos serum response element.";
 RL CELL 68:597-612(1992).
 CC -1- FUNCTION: FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR
 (SRF). REQUIRES DNA-BOUND SRF FOR TERNARY COMPLEX FORMATION AND
 MAKES EXTENSIVE DNA CONTACTS TO THE 5' SIDE OF SRF, BUT DOES NOT
 CC BIND DNA AUTONOMOUSLY.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF SAP-1 ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE, THEY ONLY DIFFER IN THE
 CC C-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M85164; G338035; -.
 DR PIR: A42093; A42093.
 DR MIM: 600246; -.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PSS0061; ETS_DOMAIN_3; 1.
 DR PRAM: PF00178; Ets; 1.
 DR HSSP: P14921; 25TW.
 DR TRANSFAC: T02128; -.
 KW DNA-BINDING: NUCLEAR PROTEIN; ALTERNATIVE SPLICING.
 FT DNA_BIND 5 85 ETS-DOMAIN.
 SQ SEQUENCE 405 AA; 44674 MW; C66EC15E CRC32;

Query Match 3.0%; Score 10; DB 1; Length 405;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 VARLWGIRKN 296
 DB 41 VARLWGIRKN 50

RESULT 10
 DEVB_MYCLE STANDARD; PRT; 247 AA.
 ID DEVB_MYCLE
 AC Q49700;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE DEVB PROTEIN HOMOLOG.
 GN DEVB OR B1486.F1.31.
 OS MYCOBACTERIUM LEPRAE.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ROBISON K., SMITH D.R.;
 RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: PUTATIVE OXIDOREDUCTASE.
 CC -1- SIMILARITY: BELONGS TO THE SOL/DEVB FAMILY.
 CC -----
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 CC -----
 DR EMBL: U00013; G466869; -.
 DR PRAM: PF0182; Glucosamine_1so; 1.
 KW OXIDOREDUCTASE.
 SQ SEQUENCE 247 AA; 26160 MW; DB677BF6 CRC32;

Query Match 2.4%; Score 8; DB 1; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 AAGAVGLE 39
 DB 224 AAGAVGLE 231

RESULT 11
 ELK1_HUMAN STANDARD; PRT; 428 AA.
 ID ELK1_HUMAN
 AC P19419;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN PROTEIN ELK-1.
 GN ELK1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89203250.
 RA RAO V.N., HUEBNER K., ISOBE M., AR-RUSHDI A., CROCE C.M.,
 RA REDDY E.S.P.;
 RT "Elk, tissue-specific ets-related genes on chromosomes X and 14 near
 RT translocation breakpoints.";
 RL SCIENCE 244:66-70(1989).
 RN [2]
 RP DOMAINS.
 RX MEDLINE: 92334979.
 RA JANKNECHT R., NORDEHM A.;
 RT "Elk-1 protein domains required for direct and SRF-assisted
 RT DNA-binding.";

```

RL NUCLEIC ACIDS RES. 20:3317-3324(1992).
CC -1- FUNCTION: MAY STIMULATE TRANSCRIPTION. BINDS TO PURINE-RICH DNA
CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: LUNG AND TESTIS.
CC -1- PTM: PHOSPHORYLATED BY THE THREE GROUPS OF MAP KINASE (P38, JNK,
CC AND ERK).
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: M25269; G538209; -
DR PIR: A41354; TVHUEK.
DR MIM: 311040; -
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PRAM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
DR TRANSFAC: T00250; -
DR NUCLEAR PROTEIN: DNA-BINDING; PHOSPHORYLATION.
DR DNA_BIND 5 86
FT SEQUENCE 428 AA; 44915 MW; 4E438DFD CRC32;
SQ

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Query Match 2.4%; Score 8; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 300 MNYDKLSR 307
DB 55 MNYDKLSR 62

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RESULT 12
ELK1_MOUSE
AC P41968; STANDARD; PRT; 429 AA.
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE ETS-DOMAIN PROTEIN ELK-1.
GN ELK1.
OS MUS MUSCULUS (MURINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL; TISSUE-EMBRYO;
RA GREVIN D., UNG S., DENHEZ F., DEHEM M., QUATANNENS B., BEGUE A.,
RA STEHELIN D., MARTIN P.;
RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDJ DATA BANKS.
RN [2]
RP SEQUENCE OF 5-224 FROM N.A.
RC TISSUE-EMBRYO;
RX MEDLINE: 95047310.
RA GIOVANE A., PINTZAS A., MAIRA S.-M., SOBIESZCZUK P., WASYLK B.;
RT "Net, a new ets transcription factor that is activated by Ras.";
RL GENES DEV. 8:1502-1513(1994).
CC -1- FUNCTION: MAY STIMULATE TRANSCRIPTION. BINDS TO PURINE-RICH DNA
CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND TO A

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CC LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: X87257; G836635; -
DR EMBL: Z36939; G535923; -
DR MGD: MG1:101833; ELK1.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PRAM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
DR NUCLEAR PROTEIN: DNA-BINDING; PHOSPHORYLATION.
DR DNA_BIND 5 86
FT SEQUENCE 429 AA; 45243 MW; F78E8069 CRC32;
SQ

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Query Match 2.4%; Score 8; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 300 MNYDKLSR 307
DB 55 MNYDKLSR 62

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RESULT 13
ELK3_HUMAN
AC P41970; STANDARD; PRT; 407 AA.
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE ETS-DOMAIN PROTEIN ELK-3 (ETS-RELATED PROTEIN NET) (SRF ACCESSORY
DE PROTEIN 2) (SAP2).
GN ELK3 OR NET.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95047310.
RA GIOVANE A., PINTZAS A., MAIRA S.-M., SOBIESZCZUK P., WASYLK B.;
RT "Net, a new ets transcription factor that is activated by Ras.";
RL GENES DEV. 8:1502-1513(1994).
CC -1- FUNCTION: MAY BE A NEGATIVE REGULATOR OF TRANSCRIPTION BUT CAN
CC ACTIVATE TRANSCRIPTION WHEN COEXPRESSED WITH RAS, SRC OR MOS.
CC FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS
CC AND SRF MOTIFS OF THE FOS SERUM RESPONSE ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.

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DR EMBL: Z36715; G531523; -
DR MIM: 600247; -
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.

DR PFAM: PF00178; Ets; 1.
 DR HSSP: P14921; 2STM.
 DR TRANSFAC: T01414; -
 DR TRANSCRIPTION REGULATION: ACTIVATOR; REPRESSOR; NUCLEAR PROTEIN;
 KW DNA-BINDING.
 FT DNA_BIND 5 85 ETS-DOMAIN.
 FT DOMAIN 207 212 POLY-ALA.
 SO SEQUENCE 407 AA; 44365 MW; D0F7E21D CRC32;

Query Match 2.4%; Score 8; DB 1; Length 407;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 300 MNYDKLSR 307
 Db 54 MNYDKLSR 61

RESULT 14
 ID ELK3_MOUSE STANDARD; PRT; 409 AA.
 AC P41971; P97747; Q62346;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN PROTEIN ELK-3 (ETS-RELATED PROTEIN NET) (ETS-RELATED
 DE PROTEIN ERP).
 GN ELK3 OR NET OR ERP.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYO;
 RX MEDLINE: 95047310.
 RA GIOVANE A., PINTAS A., MAIRA S.-M., SOBIESZCZUK P., WASYLK B.;
 RT "Net, a new ets transcription factor that is activated by Ras.";
 RL GENES DEV. 8:1502-1513(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-LUNG;
 RX MEDLINE: 94217726.
 RA LOPEZ M., OETGEN P., ARBARELI Y., DENDORFER U., LIBERMAN T.A.;
 RT "Erp, a new member of the ets transcription factor/oncoprotein
 RT B-lymphocyte development.";
 RL MOL. CELL. BIOL. 14:3292-3309(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97047916.
 RA NOZAKI M., ONISHI Y., KANNO N., ONO Y., FUJIMURA Y.;
 RT "Molecular cloning of Elk-3, a new member of the Ets family expressed
 RT during mouse embryogenesis and analysis of its transcriptional
 RT repression activity.";
 RL DNA CELL BIOL. 15:855-862(1996).
 CC -1- FUNCTION: MAY BE A NEGATIVE REGULATOR OF TRANSCRIPTION BUT CAN
 CC ACTIVATE TRANSCRIPTION WHEN COEXPRESSED WITH RAS, SRC OR MOS.
 CC FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS
 CC AND SRP MOTIFS OF THE FOS SERUM RESPONSE ELEMENT.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: HEART, LIVER, LUNG, KIDNEY AND MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 CC EMBL: 232815; G479113; -

DR EMBL: L19953; G436185; -
 DR EMBL: S82864; G1836130; -
 DR MGD: MGI:101762; ELK3.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PFAM: PF00178; Ets; 1.
 DR HSSP: Q00422; IAWC.
 DR TRANSFAC: T01413; -
 DR TRANSCRIPTION REGULATION: ACTIVATOR; REPRESSOR; NUCLEAR PROTEIN;
 KW DNA-BINDING.
 FT DNA_BIND 5 85 ETS-DOMAIN.
 FT DOMAIN 208 212 POLY-ALA.
 FT CONFLICT 152 152 O -> E (IN REF. 1).
 FT CONFLICT 199 199 M -> V (IN REF. 3).
 FT CONFLICT 238 238 A -> V (IN REF. 1).
 FT CONFLICT 331 331 A -> T (IN REF. 3).
 SO SEQUENCE 409 AA; 44445 MW; 0FB56166 CRC32;

Query Match 2.4%; Score 8; DB 1; Length 409;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 300 MNYDKLSR 307
 Db 54 MNYDKLSR 61

RESULT 15
 ID ERF_HUMAN STANDARD; PRT; 548 AA.
 AC P50548;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
 GN ERF.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96030784.
 RA SCOURAS D.N., ATHANASIOU M.A., BEAL G.J. JR., FISHER R.J., BLAIR D.G.,
 RA MAKROHALLAKIS G.J.;
 RT "Erp, an Ets domain protein with strong transcriptional repressor
 RT activity, can suppress ets-associated tumorigenesis and is regulated
 RT by phosphorylation during cell cycle and mitogenic stimulation.";
 RL EMBO J. 14:4781-4793(1995).
 CC -1- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1
 CC ELEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED
 CC IN CELLULAR PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.
 CC PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 CC EMBL: U15655; G1015337; -
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PFAM: PF00178; Ets; 1.
 DR HSSP: Q01543; IFTI.
 DR TRANSCRIPTION REGULATION: REPRESSOR; DNA-BINDING; NUCLEAR PROTEIN;
 KW

KM PHOSPHORYLATION. 107 ETS-DOMAIN.
 FT DNA_BIND 27 POLY-SER.
 FT DOMAIN 166 171 POLY-GLY.
 FT DOMAIN 290 293 POLY-SER.
 FT DOMAIN 362 373 POLY-SER.
 FT DOMAIN 418 423 POLY-PRO.
 FT DOMAIN 496 499 POLY-GLY.
 FT MOD_RES 526
 FT MUTAGEN 526
 SQ SEQUENCE 548 AA: 58776 MM: 971D7FD CRC32: T->A: LOSS OF A PHOSPHORYLATION SITE.

Query Match 2.4%; Score 8; DB 1; Length 548;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 300 MNYDKLSR 307
 DB 76 MNYDKLSR 83

Search completed: November 20, 1999, 18:05:36
 Job time: 313 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 1999, 18:00:23 ; Search time 10.28 seconds
 (without alignments)
 921.194 Million cell updates/sec

Title: US-09-126-945-2

Perfect score: 335

Sequence: 1 MGSASFGLSVSPSHLLPP.....GIIRPDISRLVQFVHP1 335

Scoring table: OLIGO

Searched: 77977 seqs, 28268293 residues

Database : SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	7.2	114	1	ETS4_DROME
2	14	4.2	510	1	ERM_HUMAN
3	14	4.2	477	1	ETV1_HUMAN
4	14	4.2	477	1	ETV1_MOUSE
5	14	4.2	551	1	ETV4_HUMAN
6	14	4.2	555	1	ETV4_MOUSE
7	10	3.0	431	1	SAPA_HUMAN
8	10	3.0	430	1	SAPA_MOUSE
9	10	3.0	405	1	SAPB_HUMAN
10	8	2.4	247	1	DEVB_MYCLE
11	8	2.4	428	1	ELK1_HUMAN
12	8	2.4	429	1	ELK1_MOUSE
13	8	2.4	407	1	ELK3_HUMAN
14	8	2.4	409	1	ELK3_MOUSE
15	8	2.4	548	1	ERF_HUMAN
16	8	2.4	551	1	ERF_MOUSE
17	8	2.4	478	1	ERG_CHICK
18	8	2.4	462	1	ERG_HUMAN
19	8	2.4	173	1	ERG_LYTV
20	8	2.4	272	1	ERG_MOUSE
21	8	2.4	64	1	ETS3_DROME
22	8	2.4	102	1	ETS6_DROME
23	8	2.4	250	1	ETV3_HUMAN
24	8	2.4	452	1	ETV1_HUMAN
25	8	2.4	452	1	ETV1_MOUSE
26	8	2.4	453	1	FLI1_XENLA
27	8	2.1	421	1	ACDM_HUMAN
28	7	2.1	421	1	ACDM_MOUSE
29	7	2.1	421	1	ACDM_PIG
30	7	2.1	421	1	ACDM_RAT
31	7	2.1	444	1	CEEG_CEPAC
32	7	2.1	686	1	CNG1_HUMAN
33	7	2.1	333	1	DCTP_RHOC
34	7	2.1	270	1	DNA_SERNA
35	7	2.1	412	1	EGR2_BRAE
36	7	2.1	619	1	EGR1_HUMAN
37	7	2.1	612	1	ELF1_MOUSE
38	7	2.1	137	1	ELF1_MOUSE
39	7	2.1	610	1	GLM1_METUA
40	7	2.1	310	1	GLM2_THIE
41	7	2.1	315	1	GTRI_YEAS
42	7	2.1	411	1	HAT3_ARAT
43	7	2.1	311	1	HOX3_BRAFL
					LB4D_HUMAN

44 7 2.1 329 1 LB4D_PIG 029073 sus scrofa
45 7 2.1 692 1 YPH5_THIIV 945365 thioyctis

ALIGNMENTS

RESULT 1

ETSA_DROME STANDARD: PRT: 114 AA.
AC P29775;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE DNA-BINDING PROTEIN D-ETS-4 (FRAGMENT).
GN ETS98B OR ETS-4.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA: METAZOA: ARTHROPODA: TRACHEATA: HEXAPODA: INSECTA:
OC PTERYGOTA: DIPTERA: BRACHYCERA: MUSCOMORPHA: EPHIROIDEA:
CC DROSOPHILIDAE: DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92249640.
RA CHEN T., BUNTING M., KARIM F.D., THUMMEL C.S.;
RT "Isolation and characterization of five Drosophila genes that encode
an ets-related DNA binding domain.";
RL DEV. BIOL. 151:176-191(1992).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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DR EMBL: M88474: G157196: -
DR PIR: S28821: S28821.
DR FLYBASE: FBgn0005659; ETS98B.
DR PROSITE: PS00345; ETS_DOMAIN_1: 1.
DR PROSITE: PS00346; ETS_DOMAIN_2: 1.
DR PROSITE: PS50061; ETS_DOMAIN_3: 1.
DR PFAM: PF00178; Ets: 1.
DR HSSP: 001543; 1FET.
KW DNA-BINDING; NUCLEAR PROTEIN.
FT NON_TER 1
FT DNA_BIND 26 108 ETS-DOMAIN.
FT NON_TER 114 114
SO SEQUENCE 114 AA: 13051 MW: E9003913 CRC32:

Query Match 7.2%; Score 24; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 24: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 294 KNRPMANTDKLSRSIROYKKGI 317
DB 71 KNRPMANTDKLSRSIROYKKGI 94

RESULT 2

ERM_HUMAN STANDARD: PRT: 510 AA.
AC P4161;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ETS-RELATED PROTEIN ERM (ETS TRANSLLOCATION VARIANT 5).
GN ETV5 OR ERM.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:

OC PRIMATES: CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE: 94203669.
RA MONTE D., BAERT J.-L., DEFOSSEZ P.-A., DE LAUNOIT Y., STEHELIN D.;
RT "Molecular cloning and characterization of human ERM, a new member of
the Ets family closely related to mouse PEA3 and ERB1 transcription
factors.";
RL ONCOGENE 9:1397-1406(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96299763.
RA MONTE D., COTTRE L., DEMITTE F., DEFOSSEZ P.-A., LE CONIAT D.,
STEHELIN R., BEGER Y., DE LAUNOIT Y.;
RT "Genomic organization of the human ERM (ETV5) gene, a PEA3 group
member of Ets transcription factors.";
RL GENOMICS 35:236-240(1996).
CC -1- FUNCTION: BINDS TO DNA SEQUENCES CONTAINING THE CONSENSUS
NUCLEOTIDE CORE SEQUENCE GGAA.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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DR EMBL: X76184: G479167: -
DR EMBL: X96381: E225719: -
DR EMBL: X96380: E225719; JOINED.
DR EMBL: X96382: E225719; JOINED.
DR EMBL: X96379: E225719; JOINED.
DR EMBL: X96378: E225719; JOINED.
DR EMBL: X96377: E225719; JOINED.
DR EMBL: X96376: E225719; JOINED.
DR EMBL: X96375: E225719; JOINED.
DR PIR: S43692; S43692.
DR MIM: 601600: -
DR PROSITE: PS00345; ETS_DOMAIN_1: 1.
DR PROSITE: PS00346; ETS_DOMAIN_2: 1.
DR PROSITE: PS50061; ETS_DOMAIN_3: 1.
DR PFAM: PF00178; Ets: 1.
DR HSSP: P14921; 2STW.
KW DNA-BINDING; NUCLEAR PROTEIN.
FT DNA_BIND 368 448 ETS-DOMAIN.
FT SEQUENCE 510 AA: 57838 MW: 75812280 CRC32:

Query Match 4.2%; Score 14; DB 1; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMANTDKLSRS 308
DB 412 KNRPMANTDKLSRS 425

RESULT 3

ETV1_HUMAN STANDARD: PRT: 477 AA.
AC P50549;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ETS TRANSLLOCATION VARIANT 1 (ERB1 PROTEIN).
GN ETV1 OR ERB1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:

CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95215084.
 RA JEON I.-S., DAVIS J.N., BRAUN B.S., SUBLETT J.E., ROUSSEL M.F.,
 RA DENNY C.T., SHAPIRO D.N.;
 RT "A variant Ewing's sarcoma translocation (7;22) fuses the EWS gene to
 the ETS gene ETV1."
 RL ONCOGENE 10:1229-1234(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE; 95380185.
 RA MONTE D., COUTTE L., BAERT J.-L., ANGELI I., STEHELIN D.,
 RA DE LAUNOIT Y.;
 RT "Molecular characterization of the ets-related human transcription
 factor ERB1."
 RL ONCOGENE 11:771-779(1995).
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
 CC CONTAINING THE CONSENSUS PENTANUCLEOTIDE 5'-CGGA(AT)-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC -1- TISSUE SPECIFICITY: VERY HIGHLY EXPRESSED IN BRAIN, HIGHLY
 CC EXPRESSED IN TESTIS, LUNG AND HEART, MODERATELY IN SPLEEN, SMALL
 CC INTESTINE, PANCREAS AND COLON, WEAKLY IN LIVER, PROSTATE AND
 CC THYMUS. VERY WEAKLY IN SKELETAL MUSCLE, KIDNEY AND OVARY AND NOT
 CC IN PLACENTA AND PERIPHERAL BLOOD LEUCOCYTES.
 CC -1- DISBASE: A FORM OF EWING'S SARCOMA IS CHARACTERIZED BY A
 CC CHROMOSOMAL TRANSLOCATION T(7;22)(P22;Q12) WHICH INVOLVES ETV1
 CC AND EWS.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL; U17163; G596006; -;
 DR EMBL; X87173; G1045061; -;
 DR MIM; 600541; -;
 DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE; PS50061; ETS_DOMAIN_3; 1.
 DR PFAM; PF00178; Ets; 1.
 DR HSSP; P14921; 2STW.
 KM TRANSCRIPTION REGULATION; ACTIVATOR; NUCLEAR PROTEIN; DNA-BINDING;
 KW PROTO-ONCOGENE; CHROMOSOMAL TRANSLOCATION.
 FT DNA_BIND 335 415
 FT CONFLICT 39 39 L -> V (IN REF. 2).
 FT CONFLICT 61 79 AQPNDNDQEPYDQASL -> V (IN REF. 2).
 FT CONFLICT 117 117 S -> C (IN REF. 2).
 FT CONFLICT 127 127 N -> K (IN REF. 2).
 FT CONFLICT 253 253 MISSING (IN REF. 2).
 FT CONFLICT 349 349 S -> A (IN REF. 2).
 SO SEQUENCE 477 AA; 55100 MW; 75BD7133 CRC32;

Query Match 4.2% Score 14; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNRPMNNDKLSRS 308
 DB 379 KNRPMNNDKLSRS 392

RESULT 4
 ETV1_MOUSE STANDARD; PRT; 477 AA.
 ID ETV1_MOUSE
 AC P1164;
 RA 01-FEB-1995 (REL. 31, CREATED)

DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ERB1 PROTEIN (ETS TRANSLOCATION VARIANT 1).
 GN ETV1 OR ETSR81 OR ERB1.
 OS MUS MUSCULUS (MUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC MURIDAE; SCIROGNATHI; MORIDAE; MORINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYO;
 RX MEDLINE; 94040714.
 RA BROWN T.A., MCKNIGHT S.L.;
 RT "Specificities of protein-protein and protein-DNA interaction of GABP
 alpha and two newly defined ets-related proteins."
 RL GENES DEV. 6:2502-2512(1992).
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
 CC CONTAINING THE CONSENSUS PENTANUCLEOTIDE 5'-CGGA(AT)-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN KIDNEY, MODERATE LEVELS SEEN IN
 CC THE HEART, BRAIN, LUNG, EMBRYO AND LOWER LEVELS SEEN IN SPLEEN,
 CC INTESTINE, TESTIS AND THYMUS.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC -----
 DR EMBL; L10426; G515964; -;
 DR PIR; B46396; B46396;
 DR MGI; M92954; ETSR81.
 DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE; PS50061; ETS_DOMAIN_3; 1.
 DR PFAM; PF00178; Ets; 1.
 DR HSSP; P14921; 2STW.
 KM TRANSCRIPTION REGULATION; NUCLEAR PROTEIN; DNA-BINDING.
 FT DNA_BIND 335 415
 SO SEQUENCE 477 AA; 55040 MW; 670ADC77 CRC32;

Query Match 4.2% Score 14; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNRPMNNDKLSRS 308
 DB 379 KNRPMNNDKLSRS 392

RESULT 5
 ETV4_HUMAN STANDARD; PRT; 551 AA.
 ID ETV4_HUMAN
 AC P43268;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ADENOVIRUS ELA ENHANCER BINDING PROTEIN (ELA-E) (ETS TRANSLOCATION
 DE VARIANT 4) (FRAGMENT).
 GN ETV4 OR ELAF.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 95293380.
 RA FRIEDMAN L.S., OSTERMEYER E.A., LYNCH E.D., SZABO C.I., MEZA J.E.,
 RA ANDERSON L.A., DOWD P., LEE M.K., ROWELL S.E., ELLISON J.,
 RA BOYD J., KING M.C.;
 RT "22 genes from chromosome 17q21: cloning, sequencing, and

RT characterization of mutations in breast cancer families and tumors.";
 RL GENOMICS 25:256-263(1995).
 RN [2]
 RP SEQUENCE OF 90-551 FROM N.A.
 RX MEDLINE: 93181246.
 RA HIGASHINO F., YOSHIDA K., FUJINAGA K., KAMIO K., FUJINAGA K.;
 RT "Isolation of a cDNA encoding the adenovirus E1A enhancer binding
 RT protein: a new human member of the ets oncogene family.";
 RL NUCLEIC ACIDS RES. 21:547-553(1993)
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE ENHANCER OF
 CC THE ADENOVIRUS E1A GENE; THE CORE-BINDING SEQUENCE IS
 CC 5' (ACGGA)ATGT-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC -----
 DR EMBL: U18018; G602288; -;
 DR EMBL: D12765; G219611; -;
 DR MIM: 600711; -;
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PFAM: PF00178; Ets; 1.
 DR HSP: P14921; 25TW.
 DR TRANSFAC: T00685; -;
 KW DNA-BINDING; NUCLEAR PROTEIN; ACTIVATOR; TRANSCRIPTION REGULATION.
 FT NON_TER 1 1
 FT DOMAIN 116 142 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 215 311 GLN-RICH.
 FT DNA_BIND 408 488 ETS-DOMAIN.
 FT CONFLICT 91 94 GNGS -> EMSD (IN REF. 2).
 SQ SEQUENCE 551 AA: 60570 MW: 11805840 CRC32:

Query Match 4.2%; Score 14; DB 1; Length 551;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMANYDKLSRS 308
 DB 452 KNRPMANYDKLSRS 465
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RESULT 6
 ID ETV4_MOUSE STANDARD: PRT; 555 AA.
 AC P28322;
 DT 01-DEC-1992 (REL. 24, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE POLYOMAVIRUS ENHANCER ACTIVATOR 3 (PEA3 PROTEIN) (ETS TRANSLLOCATION
 DE VARIANT 4).
 GN ETV4 OR PEA3 OR PEA-3.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC ROENTIIA; SCUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92192459.
 RA XIN J.-H., COMIE A., LACHANCE P., HASSELL J.A.;
 RT "Molecular cloning and characterization of PEA3, a new member of the
 RT Ets oncogene family that is differentially expressed in mouse
 RT embryonic cells.";
 RL GENES DEV. 6:481-496(1992).
 CC -1- FUNCTION: BINDS TO THE PEA3 MOTIF (5'-AGGAG-3'). MAY PLAY A
 CC REGULATORY ROLE DURING EMBRYOGENESIS.

CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: EPIDIDYMIS AND THE BRAIN.
 CC -1- PTM: PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: X63190; G53628; -;
 DR PIR: S24061; S24061.
 DR MGD: MGT:99423; PEA3.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PFAM: PF00178; Ets; 1.
 DR HSP: P14921; 25TW.
 DR TRANSFAC: T00684; -;
 KW DNA-BINDING; NUCLEAR PROTEIN; ACTIVATOR; TRANSCRIPTION REGULATION;
 KW PHOSPHORYLATION.
 FT DOMAIN 124 150 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 217 315 GLN-RICH.
 FT DNA_BIND 412 492 ETS-DOMAIN.
 SQ SEQUENCE 555 AA: 60846 MW: 084570E CRC32:

Query Match 4.2%; Score 14; DB 1; Length 555;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMANYDKLSRS 308
 DB 456 KNRPMANYDKLSRS 469
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RESULT 7
 ID SAPA_HUMAN STANDARD: PRT; 431 AA.
 AC P28324;
 DT 01-DEC-1992 (REL. 24, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (SAP-1A) (ETS-DOMAIN
 DE PROTEIN ELK-4).
 GN ELK4 OR SAP1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92154673.
 RA DALTON S., TREISMAN R.;
 RT "Characterization of SAP-1, a protein recruited by serum response
 RT factor to the c-fos serum response element.";
 RL CELL 68:597-612(1992).
 CC [2]
 CC REVISIONS.
 RP MEDLINE: 94123347.
 RA DALTON S., TREISMAN R.;
 RT "Characterization of SAP-1, a protein recruited by serum response
 RT factor to the c-fos serum response element.";
 RL CELL 76:411-411(1994).
 CC -1- FUNCTION: FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR
 CC (SRF). REQUIRES DNA-BOUND SRF FOR TERNARY COMPLEX FORMATION AND
 CC MAKES EXTENSIVE DNA-CONTACTS TO THE 5' SIDE OF SRF, BUT DOES NOT
 CC BIND DNA AUTONOMOUSLY.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF SAP-1 ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE, THEY ONLY DIFFER IN THE

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CC C-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: M85165; G429186; -
DR PIR: B42093; B42093.
DR MIM: 600246; -
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS00061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
DR TRANSFAC: T00737; -
DR DNA-BINDING: NUCLEAR PROTEIN: ALTERNATIVE SPLICING.
DR DNA_BIND 5 ETS-DOMAIN
FT SEQUENCE 431 AA: 46827 MW: 2860052A CRC32:

Query Match 3.0%; Score 10; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 VARLWGIRKN 296
DB 41 VARLWGIRKN 50

RESULT 8
SAPA_MOUSE STANDARD; PRT; 430 AA.
ID SAPA_MOUSE
AC P41158;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (SAP-1A) (ETS-DOMAIN
DE PROTEIN ELK-4).
GN ELK4 OR SAP1.
OS MUS MUSCULUS (MUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCURIONATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYO;
RX MEDLINE: 95047310.
RA GIOVANE A., PINTZAS A., MAIRA S.-M., SOBIESZCZUR P., WASYLAK B.;
RT "Net, a new ets transcription factor that is activated by Ras.";
RL GENES DEV. 8:1502-1513(1994).
CC -1- FUNCTION: CAN FORM A TERNARY COMPLEX WITH THE SRPM RESPONSE
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: LUNG AND LIVER.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: Z36885; G535128; -
DR MGD: MGI:102853; ELK4.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.

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DR PROSITE: PS00061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
DR DNA-BINDING: NUCLEAR PROTEIN.
FT DNA_BIND 5 ETS-DOMAIN.
SQ SEQUENCE 430 AA: 46867 MW: BE175C95 CRC32:

Query Match 3.0%; Score 10; DB 1; Length 430;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 VARLWGIRKN 296
DB 41 VARLWGIRKN 50

RESULT 9
SAPB_HUMAN STANDARD; PRT; 405 AA.
ID SAPB_HUMAN
AC P28323;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1B (SAP-1B) (ETS-DOMAIN
DE PROTEIN ELK-4).
GN ELK4 OR SAP1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 92154673.
RA DALTON S., TREISMAN R.;
RT "Characterization of SAP-1, a protein recruited by serum response
RT factor to the c-fos serum response element.";
RL CELL 68:597-612(1992).
CC -1- FUNCTION: FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR
CC (SRF). REQUIRES DNA-BOUND SRF FOR TERNARY COMPLEX FORMATION AND
CC MAKES EXTENSIVE DNA CONTACTS TO THE 5' SIDE OF SRF, BUT DOES NOT
CC BIND DNA AUTONOMOUSLY.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF SAP-1 ARE PRODUCED BY
CC C-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: M85164; G338035; -
DR PIR: A42093; A42093.
DR MIM: 600246; -
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS00061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
DR TRANSFAC: T02128; -
DR DNA-BINDING: NUCLEAR PROTEIN: ALTERNATIVE SPLICING.
FT DNA_BIND 5
SQ SEQUENCE 405 AA: 44674 MW: C66EC13E CRC32:

Query Match 3.0%; Score 10; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 287 VARLMGIRKN 296
DB 41 VARLMGIRKN 50

RESULT 10
DEVB_MYCLE STANDARD: PRT: 247 AA.
ID DEVB_MYCLE STANDARD: PRT: 247 AA.
AC 049700.
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DEVB OR B1496.F1.31.
GN MYCOBACTERIUM LEPRAE.
OS MYCOBACTERIUM LEPRAE.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; CORINEBACTERIINAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RA ROBISON K., SMITH D.R.;
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: PUTATIVE OXIDOREDUCTASE.
CC -1- SIMILARITY: BELONGS TO THE SOL/DEVB FAMILY.
CC -----
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CC -----
CC EMBL: U00013; G46869;
DR PFAM: PF01182; Glucosamine_1so: 1.
DR OXIDOREDUCTASE.
KW SEQUENCE 247 AA; 26160 MW; DB67BF6 CRC32;
SO

Query Match 2.4%; Score 8; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 AAGAVGLE 39
DB 224 AAGAVGLE 231

RESULT 11
ELK1_HUMAN STANDARD: PRT: 428 AA.
ID ELK1_HUMAN STANDARD: PRT: 428 AA.
AC P19419;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ETS-DOMAIN PROTEIN ELK-1.
GN ELK1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA RAO V.N., HUBNER K., ISOBE M., AR-RUSHDI A., CROCE C.M.,
RA REDDY E.S.P.;
RT "elk, tissue-specific ets-related genes on chromosomes X and 14 near
RT translocation breakpoints.";
RL SCIENCE 244:56-70(1989).
RN [2]
RP DOMAINS: 92334979.
RA JANNENCHT R., NORDHEIM A.;
RT "Elk-1 protein domains required for direct and SRF-assisted
RT DNA-binding.";
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RL NUCLEIC ACIDS RES. 20:3317-3324(1992).
CC -1- FUNCTION: MAY STIMULATE TRANSCRIPTION. BINDS TO PURINE-RICH DNA
CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: LUNG AND TESTIS.
CC -1- PTM: PHOSPHORYLATED BY THE THREE GROUPS OF MAP KINASE (P38, JNK,
CC AND ERK).
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
CC EMBL: M25269; G538209;
DR PIR: A41354; TVHUK.
DR MIM: 311040;
DR PROSITE: PS00345; ETS_DOMAIN_1: 1.
DR PROSITE: PS00346; ETS_DOMAIN_2: 1.
DR PROSITE: PS50061; ETS_DOMAIN_3: 1.
DR PFAM: PF00178; ETS: 1.
DR HSSP: P14921; 2STW.
DR TRANSFAC: T00250;
DR NUCLEAR PROTEIN: DNA-BINDING; PHOSPHORYLATION.
KW DNA_BIND 5 ETS-DOMAIN.
FT SEQUENCE 428 AA; 44915 MW; 4E438DFD CRC32;
SO

Query Match 2.4%; Score 8; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 MNYDKLSR 307
DB 55 MNYDKLSR 62

RESULT 12
ELK1_MOUSE STANDARD: PRT: 429 AA.
ID ELK1_MOUSE STANDARD: PRT: 429 AA.
AC P41969;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ETS-DOMAIN PROTEIN ELK-1.
GN ELK1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL; TISSUE-EMBRYO;
RA GREVIN D., UNG S., DENHEZ F., DEHEM M., QOUTANNEUS B., BEGUE A.,
RA STEHELIN D., MARTIN P.;
RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 5-224 FROM N.A.
RC TISSUE-EMBRYO;
RX MEDLINE: 95047310.
RA GIOVANE A., PINTZAS A., MAIRA S.-M., SOBIESZCZUK P., WASLYK B.;
RT "Net, a new ets transcription factor that is activated by Ras.";
RL GENES DEV. 8:1502-1513(1994).
CC -1- FUNCTION: MAY STIMULATE TRANSCRIPTION. BINDS TO PURINE-RICH DNA
CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC ELEMENT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND TO A
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CC LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: X87257; G836635; -
 DR EMBL: Z36939; G535923; -
 DR MGI: 101833; ELK1.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PFAM: PF00178; Ets; 1.
 DR HSSP: P14921; 2STW.
 KM NUCLEAR PROTEIN; DNA-BINDING; PHOSPHORYLATION.
 FT DNA_BIND 5 86 ETS-DOMAIN.
 FT CONFLICT 133 133 P->T (IN REF. 2).
 FT SEQUENCE 429 AA; 45243 MW; F78E8069 CRC32;
 SQ
 Query Match 2.4%; Score 8; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 300 MNYDKLSR 307
 Db 55 MNYDKLSR 62
 RESULT 13
 ELK3_HUMAN
 ID ELK3_HUMAN STANDARD; PRT; 407 AA.
 AC P41970.
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN PROTEIN ELK-3 (ETS-RELATED PROTEIN NET) (SRF ACCESSORY
 DE PROTEIN 2) (SAP2).
 GN ELK3 OR NET.
 OS HOMO SAPIENS (HUMAN).
 OC EUMAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95047310.
 RA GIOVANE A., PINTZAS A., MAIRA S.-M., SOBIESZCZUK P., WASLYK B.;
 RT "Net, a new ets transcription factor that is activated by Ras.";
 RL GENES DEV. 8:1502-1513(1994).
 CC -1- FUNCTION: MAY BE A NEGATIVE REGULATOR OF TRANSCRIPTION BUT CAN
 CC ACTIVATE TRANSCRIPTION WHEN COEXRESSED WITH RAS. SRC OR MOS
 CC FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS
 CC AND SRF MOTIFS OF THE FOS SERUM RESPONSE ELEMENT.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: Z36715; G531523; -
 DR MIM: 600247; -
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.

DR PFAM: PF00178; Ets; 1.
 DR HSSP: P14921; 2STW.
 DR TRANSFAC: T01414; -
 KM TRANSCRIPTION REGULATION; ACTIVATOR; REPRESSOR; NUCLEAR PROTEIN;
 FT DNA_BIND 5 85 ETS-DOMAIN.
 FT DNA_BIND 207 212 POLY-ALA.
 FT DOMAIN 407 AA; 44365 MW; D0F7E21D CRC32;
 SQ SEQUENCE 407 AA; 44365 MW; D0F7E21D CRC32;
 Query Match 2.4%; Score 8; DB 1; Length 407;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 300 MNYDKLSR 307
 Db 54 MNYDKLSR 61
 RESULT 14
 ELK3_MOUSE
 ID ELK3_MOUSE STANDARD; PRT; 409 AA.
 AC P41971; P97747; Q62346;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN PROTEIN ELK-3 (ETS-RELATED PROTEIN NET) (ETS-RELATED
 DE PROTEIN ERP).
 GN ELK3 OR NET OR ERP.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIDROGNATHI; MURIDAE; MORINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYO;
 RX MEDLINE: 95047310.
 RA GIOVANE A., PINTZAS A., MAIRA S.-M., SOBIESZCZUK P., WASLYK B.;
 RT "Net, a new ets transcription factor that is activated by Ras.";
 RL GENES DEV. 8:1502-1513(1994).
 CC -1- FUNCTION: MAY BE A NEGATIVE REGULATOR OF TRANSCRIPTION BUT CAN
 CC ACTIVATE TRANSCRIPTION WHEN COEXRESSED WITH RAS. SRC OR MOS.
 CC FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS
 CC AND SRF MOTIFS OF THE FOS SERUM RESPONSE ELEMENT.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: HEART, LIVER, LUNG, KIDNEY AND MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: Z32815; G479113; -

DR EMBL: L19953: G436185: -
 DR EMBL: S82864: G1836130: -
 DR MGD: MGI:101762: ELK3.
 DR PROSITE: PS00345: ETS_DOMAIN_1: 1.
 DR PROSITE: PS00346: ETS_DOMAIN_2: 1.
 DR PROSITE: PS50061: ETS_DOMAIN_3: 1.
 DR PFM: PFM0178: Ets: 1.
 DR HSP: 000422: LMC.
 DR TRANSFAC: T01413: -
 KM TRANSCRIPTION REGULATION; ACTIVATOR; REPRESSOR; NUCLEAR PROTEIN;
 KM DNA-BINDING.
 FT DNA_BIND 5 ETS-DOMAIN.
 FT DOMAIN 208 212 POLY-ALA.
 FT CONFLICT 152 152 O -> E (IN REF. 1).
 FT CONFLICT 199 199 M -> V (IN REF. 3).
 FT CONFLICT 238 238 A -> T (IN REF. 1).
 FT CONFLICT 331 331 A -> T (IN REF. 3).
 SQ SEQUENCE 409 AA: 44445 MW: 9FB56166 CRC32;

Query Match 2.4%; Score 8; DB 1; Length 409;
 Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MNYDKLSR 307
 |||||

DB 54 MNYDKLSR 61

RESULT 15
 ERF_HUMAN
 ID ERF_HUMAN STANDARD: PRT; 548 AA.
 AC P50549:
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
 GN ERF.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 96030784.
 RA SCOURAS D.N., ATHANASIOU M.A., BEAL G.J. JR., FISHER R.J., BLAIR D.G.,
 MAYNOTALASSITIS G.J.;
 RT "ERF: an ETS domain protein with strong transcriptional repressor
 activity, can suppress ets-associated tumorigenesis and is regulated
 by phosphorylation during cell cycle and mitogenic stimulation.";
 RL EMBL J. 14:4781-4793(1995).
 CC -1- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1
 ELEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED
 IN CELLULAR PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.
 CC PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC
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 CC
 CC EMBL: U15655: G1015337: -
 DR PROSITE: PS00345: ETS_DOMAIN_1: 1.
 DR PROSITE: PS00346: ETS_DOMAIN_2: 1.
 DR PROSITE: PS50061: ETS_DOMAIN_3: 1.
 DR PFM: PFM0178: Ets: 1.
 DR HSP: 001543: LFLI.
 DR TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING; NUCLEAR PROTEIN;

KW PHOSPHORYLATION.
 FT DNA_BIND 27 107 ETS-DOMAIN.
 FT DOMAIN 166 171 POLY-SER.
 FT DOMAIN 290 293 POLY-GLY.
 FT DOMAIN 362 373 POLY-SER.
 FT DOMAIN 418 423 POLY-PRO.
 FT DOMAIN 496 499 POLY-GLY.
 FT MOD_RES 526 526 PHOSPHORYLATION (BY ERK2).
 FT MUTAGEN 526 526 T->A: LOSS OF A PHOSPHORYLATION SITE.
 SQ SEQUENCE 548 AA: 58776 MW: 971D7F6D CRC32;

Query Match 2.4%; Score 8; DB 1; Length 548;
 Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MNYDKLSR 307
 |||||

DB 76 MNYDKLSR 83

Search completed: November 20, 1999, 18:05:36
 Job time: 313 sec

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OM protein - protein search, using sw model

Run on: November 20, 1999, 18:00:23 ; Search time 10.28 seconds

(without alignments)
 921.194 Million cell updates/sec

Title: US-09-126-945-2

Perfect score: 335

Sequence: 1 MGSASPGLSSVSPSHLLPP.....GIIRKPDISQRLVYQFVHP1 335

Scoring table: OIIGO

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	7.2	114	1	ETS4_DROME
2	14	4.2	510	1	ERM_HUMAN
3	14	4.2	477	1	ETV1_HUMAN
4	14	4.2	477	1	ETV1_MOUSE
5	14	4.2	551	1	ETV4_HUMAN
6	14	4.2	555	1	ETV4_MOUSE
7	10	3.0	431	1	SAPA_HUMAN
8	10	3.0	430	1	SAPA_MOUSE
9	10	3.0	405	1	SAPB_HUMAN
10	8	2.4	247	1	DEVB_HUMAN
11	8	2.4	428	1	ELK1_MOUSE
12	8	2.4	429	1	ELK1_HUMAN
13	8	2.4	407	1	ELK3_MOUSE
14	8	2.4	409	1	ELK3_HUMAN
15	8	2.4	548	1	ERF_HUMAN
16	8	2.4	551	1	ERF_MOUSE
17	8	2.4	478	1	ERG_CHICK
18	8	2.4	462	1	ERG_HUMAN
19	8	2.4	173	1	ERG_LYTV

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20      8      2  4      272  1      ERG_MOUSE
21      8      2  4      64  1      ETS3_DROME
22      8      2  4      102  1      ETS6_DROME
23      8      2  4      250  1      ETV3_HUMAN
24      8      2  4      452  1      FLI1_HUMAN
25      8      2  4      452  1      FLI1_MOUSE
26      8      2  4      453  1      FLI1_XENLA
27      7      2  1      421  1      ACDM_HUMAN
28      7      2  1      421  1      ACDM_MOUSE
29      7      2  1      421  1      ACDM_PIG
30      7      2  1      421  1      ACDM_RAT
31      7      2  1      444  1      CERG_CEPAC
32      7      2  1      386  1      CNG1_HUMAN
33      7      2  1      333  1      DCTP_RHOCA
34      7      2  1      412  1      DMA_SERMA
35      7      2  1      412  1      EGR2_BRARE
36      7      2  1      619  1      ELF1_HUMAN
37      7      2  1      612  1      ELF1_MOUSE
38      7      2  1      157  1      FKBP_METJA
39      7      2  1      610  1      GLMS_THIFE
40      7      2  1      310  1      GTRL_YEAST
41      7      2  1      315  1      HAT3_ARATH
42      7      2  1      411  1      HOS3_BRAF
43      7      2  1      311  1      LBAD_HUMAN
44      7      2  1      329  1      LBAD_PIG
45      7      2  1      692  1      YPH5_THIIV

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ALIGNMENTS

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P81270 mus musculus
P29774 drosophila
P29776 drosophila
P41162 homo sapien
O01543 homo sapien
P26323 mus musculus
P41157 xenopus lae
P11110 homo sapien
P45952 mus musculus
P41367 sus scrofa
P08503 rattus norv
P39058 cephalospor
P29973 homo sapien
P33735 rhodobacter
P45454 serralia ma
O05159 brachydanio
P32519 homo sapien
O60775 mus musculus
O57726 methanococc
O56275 t gluccosam
O00582 saccharomyc
P46602 atreidiopsis
P50901 brachioslo
O14914 homo sapien
O23073 sus scrofa
P45365 thio cystis

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RESULT 1
ETS4_DROME STANDARD: PRT: 114 AA.
ID ETS4_DROME
AC P29775;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE DNA-BINDING PROTEIN D-ETS-4 (FRAGMENT).
GN ETS98B OR ETS-4.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYTROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92249640.
RA CHEN T., BUNTING M., KARIM F.D., THUMMEL C.S.;
RT "Isolation and characterization of five Drosophila genes that encode
  an ets-related DNA binding domain."
RL DEV. BIOL. 151:176-191(1992).

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CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----

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DR EMBL: M88474. G157196; -.
DR PIR: S28821. S28821.
DR FLYBASE: FBgn0005659; Ets98B.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSSP: O01543; 1FLI.
DR DNA-BINDING: NUCLEAR PROTEIN.
KW DNA_BIND 26 108 ETS_DOMAIN.
FT

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FT NON_TER 114 114
SQ SEQUENCE 114 AA; 13051 MW; E9003913 CRC32.

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Query Match 7.28; Score 24; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 294 RKNRPANMYDKLSIRQYKGI 317
DB 71 RKNRPANMYDKLSIRQYKGI 94

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RESULT 2

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ID ERM_HUMAN STANDARD: PRT: 510 AA.
AC P41161;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ETS-RELATED PROTEIN ERM (ETS TRANSLLOCATION VARIANT 5).
GN ETV5 OR ERM.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-TESTIS;
RX MEDLINE: 94203669.
RA MONTE D., BAERT J.-L., DEFOSSER P.-A., DE LAUNOIT Y.,
RT "Molecular cloning and characterization of human ERM,
  a new member of
  the Ets family closely related to mouse PEA3 and ERB1 transcription
  factors."
RL ONCOGENE 9:1397-1406(1994).

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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96299763.
RA MONTE D., COUTTE L., DEWITTE F., DEFOSSER P.-A., LE CONIAT D.,
RA STEHELIN R., BERGER Y., DE LAUNOIT Y.,
RT "Genomic organization of the human ERM (ETV5) gene, a PEA3 group
  member of Ets transcription factors."
RL GENOMICS 35:236-240(1996).

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```

CC -1- FUNCTION: BINDS TO DNA SEQUENCES CONTAINING THE CONSENSUS
CC NUCLEOTIDE CORE SEQUENCE GGAA.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----

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DR EMBL: X76184. G479167; -.
DR EMBL: X96381. E225719; -.
DR EMBL: X96380. E225719; JOINED.
DR EMBL: X96382. E225719; JOINED.
DR EMBL: X96379. E225719; JOINED.
DR EMBL: X96378. E225719; JOINED.
DR EMBL: X96377. E225719; JOINED.
DR EMBL: X96376. E225719; JOINED.
DR EMBL: X96375. E225719; JOINED.
DR PIR: S43692; S43692.
DR MIM: 601600; -.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PFAM: PF00178; Ets; 1.
DR HSSP: P14921; 25TW.
DR DNA-BINDING: NUCLEAR PROTEIN.
KW

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FT   DNA_BIND      368      448      ETS-DOMAIN.
SQ   SEQUENCE      510 AA: 57938 MW: 7581228D CRC32:
                                4.2%; Score 14; DB 1; Length 510;
Query Match      100.0%; Pred. No. 1.9e-06;
Best Local Similarity
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      295 KNRPMANWDKLSRS 308
          |||||
DB      412 KNRPMANWDKLSRS 425

RESULT      3
ETV1_HUMAN  STANDARD:      PRT: 477 AA.
ID      AC      P50549;
DT      01-OCT-1996 (REL. 34, CREATED)
DT      01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT      01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE      ETS TRANSLLOCATION VARIANT 1 (ERB1 PROTEIN).
GN      ETV1 OR ERB1.
NC      HOMO SAPIENS (HUMAN).
CC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC      PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN      [1]
RX      MEDLINE: 95215084.
RA      JEON I.-S., DAVIS J.N., BRAUN B.S., SUBLETT J.E., ROUSSEL M.F.,
RA      DENNY C.T., SHAPIRO D.N.;
RT      "A variant Ewing's sarcoma translocation (7:22) fuses the EWS gene to
RT      the ETS gene ETV1."
RL      ONCOGENE 10:1229-1234(1995).
RN      [2]
RX      SEQUENCE FROM N.A.
RA      TISSUE-KIDNEY;
RA      MEDLINE: 95380185.
RA      MONTE D., COOTTE L., BAERT J.-L., ANGELI I., STEHSELIN D.,
RA      DE LAUNOIT Y.;
RT      "Molecular characterization of the ets-related human transcription
RT      factor ERB1."
RL      ONCOGENE 11:771-779(1995).
CC      -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
CC      CONTAINING THE CONSENSUS PENTANUCLEOTIDE 5'-CGGAAAT-3'.
CC      -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC      -1- TISSUE SPECIFICITY: VERY HIGHLY EXPRESSED IN BRAIN, SPLEEN,
CC      EXPRESSED IN TESTIS, LUNG AND HEART. MODERATELY IN GLYCE, SMALL
CC      INTESTINE, PANCREAS AND COLON. WEAKLY IN LIVER, PROSTATE AND
CC      THYMUS, VERY WEAKLY IN SKELETAL MUSCLE, KIDNEY AND OVARY AND NOT
CC      IN PLACENTA AND PERIPHERAL BLOOD LEUKOCYTES.
CC      -1- DISEASE: A FORM OF EWING'S SARCOMA IS CHARACTERIZED BY A
CC      CHROMOSOMAL TRANSLLOCATION T(7;22)(P22;Q12) WHICH INVOLVES ETV1
CC      AND EWS.
CC      -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
-----
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CC      or send an email to license@sdb.ch.
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DR      EMBL: U17163; G596006;
DR      EMBL: X87175; G1045061;
DR      MIM: 600541;
DR      PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR      PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR      PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR      Pfam: PF00178; Ets; 1.
DR      HSPB: P14821; 25TW.
KW      TRANSCRIPTION REGULATION; ACTIVATOR; NUCLEAR PROTEIN; DNA-BINDING;
KW      PROTO-ONCOGENE; CHROMOSOMAL TRANSLLOCATION.

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FT   DNA_BIND      335      415      ETS-DOMAIN.
FT   CONFLICT      39       39       L -> V (IN REF. 2).
FT   CONFLICT      61       79       AQVNDNDQEPFDYQASL -> V (IN REF. 2).
FT   CONFLICT      117      117      S -> C (IN REF. 2).
FT   CONFLICT      127      127      N -> K (IN REF. 2).
FT   CONFLICT      253      253      MISSING (IN REF. 2).
FT   CONFLICT      349      349      S -> A (IN REF. 2).
SO   SEQUENCE      477 AA; 55100 MW; 75BD133 CRC32;

Query Match      4.28; Score 14; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 1,7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  295  KNRPMANTDKLSRS 308
      |||||
Db   379  KNRPMANTDKLSRS 392

RESULT 4
ETV1_MOUSE STANDARD: PRT: 477 AA.
ID   ETV1_MOUSE
AC   P41164;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   ERB1 PROTEIN (ETS TRANSLOCATION VARIANT 1)...
GN   ETV1 OR ETSRP81 OR ER81.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC   RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE-EMBRYO.
RX   MEDLINE: 94040714.
RA   BROWN T.A., MCKNIGHT S.L.;
RT   "Specificities of protein-protein and protein-DNA interaction of GABP
RT   alpha and two newly defined ets-related proteins."
RL   GENES DEV. 6:2502-2512(1992).
CC   -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO DNA SEQUENCES
CC   CONTAINING THE CONSENSUS PERNANCTOCTIDE 5'-CGCATAT]-3'.
CC   -1- SUBCELLULAR LOCATION: NUCLEAR.
CC   -1- TISSUE SPECIFICITY: ABUNDANT IN KIDNEY. MODERATE LEVELS SEEN IN
CC   THE HEART, BRAIN, LUNG, EMBRYO AND LOWER LEVELS SEEN IN SPLEEN,
CC   INTESTINE, TESTIS AND THYMUS.
CC   -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
-----
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CC   or send an email to license@sib.ch).
CC   -----
DR   EMBL: L10426; G515964; -
DR   PIR: B46396; B46396.
DR   MGD: MGI:99254; ETSRP81.
DR   PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR   PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR   PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR   Pfam: PF00178; Ets; 1.
DR   HSP: P14921; 25TW.
DR   TRANSCRIPTION REGULATION: NUCLEAR PROTEIN; DNA-BINDING.
KM   DNA_BIND 335 415 ETS-DOMAIN.
SO   SEQUENCE 477 AA; 55040 MW; 670ADC77 CRC32;

Query Match      4.28; Score 14; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 1,7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  295  KNRPMANTDKLSRS 308

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Db 379 KNRPANMYDKLSRS 392

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RESULT 5
ID ETV4_HUMAN STANDARD: PRT: 551 AA.
AC P28322;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE POLYOMAVIRUS ENHANCER ACTIVATOR 3 (PEA3 PROTEIN) (ETS TRANSLLOCATION
DE VARIANT 4) (FRAGMENT).
GN ETV4 OR EIAF.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95293380.
RA FRIDMAN L.S., OSTERMEYER E.A., LYNCH E.D., SZABO C.I., MEZA J.E.,
RA ANDERSON L.A., DOWD P., LEE M.K., ROWELL S.E., ELISON J.,
RA BOYD J., KING M.C.,
RT "22 genes from chromosome 17q21: cloning, sequencing, and
RT characterization of mutations in breast cancer families and tumors."
RL GENOMICS 25:256-263(1995).
RN [2]
RP SEQUENCE OF 90-551 FROM N.A.
RX MEDLINE: 93181246.
RA HIGASHINO F., YOSHIDA K., FUJINAGA K., KAMIO K., FUJINAGA K.;
RT "Isolation of a cDNA encoding the adenovirus E1A enhancer binding
RT protein: a new human member of the ets oncogene family."
RL NUCLEIC ACIDS RES. 21:547-553(1993).
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE ENHANCER OF
CC THE ADENOVIRUS E1A GENE; THE CORE-BINDING SEQUENCE IS
CC 5'ACGCGAATGCT-3'.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -----
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CC -----
DR EMBL: U18018; G602288;
DR EMBL: D12765; G219611;
DR MIM: 600711;
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PFM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
DR TRANSFAC: T00685;
KM DNA-BINDING; NUCLEAR PROTEIN; ACTIVATOR; TRANSCRIPTION REGULATION.
FT NON_TER 1 1
FT DOMAIN 116 142 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 215 311 GLN-RICH.
FT DNA_BIND 408 488 ETS-DOMAIN.
FT CONFLICT 91 94 GNCS -> EMSD (IN REF. 2).
SQ SEQUENCE 551 AA; 60570 MW; 1F8D5E40 CRC32;

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Query Match 4.28; Score 14; DB 1; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 295 KNRPANMYDKLSRS 308
Db 452 KNRPANMYDKLSRS 465

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RESULT 6
ID ETV4_MOUSE STANDARD: PRT: 555 AA.
AC P28322;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DE POLYOMAVIRUS ENHANCER ACTIVATOR 3 (PEA3 PROTEIN) (ETS TRANSLLOCATION
DE VARIANT 4).
GN ETV4 OR PEA3 OR PEA-3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92192459.
RA XIN J.-H., COMIE A., LACHANCE P., HASSELL J.A.;
RT "Molecular cloning and characterization of PEA3, a new member of the
RT Ets oncogene family that is differentially expressed in mouse
RT embryonic cells."
RL GENES DEV. 6:481-496(1992).
CC -1- FUNCTION: BINDS TO THE PEA3 MOTIF (5'-AGGAG-3'). MAY PLAY A
CC REGULATORY ROLE DURING EMBRYOGENESIS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: EPIDIDYMI AND THE BRAIN.
CC -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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CC -----
DR EMBL: X63190; G53628;
DR PIR: S24061; S24061.
DR MGD: MGI:99423; PEA3.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
DR PFM: PF00178; Ets; 1.
DR HSSP: P14921; 2STW.
DR TRANSFAC: T00684;
KM DNA-BINDING; NUCLEAR PROTEIN; ACTIVATOR; TRANSCRIPTION REGULATION;
KM PHOSPHORYLATION.
FT DOMAIN 124 150 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 217 315 GLN-RICH.
FT DNA_BIND 412 492 ETS-DOMAIN.
SQ SEQUENCE 555 AA; 60846 MW; 084F57CE CRC32;

```

Query Match 4.28; Score 14; DB 1; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 295 KNRPANMYDKLSRS 308
Db 456 KNRPANMYDKLSRS 469

RESULT 7
ID SAPA_HUMAN STANDARD: PRT: 431 AA.
AC P28324;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (SAP-1A) (ETS-DOMAIN
DE PROTEIN ELK-4).
GN ELK4 OR SAP1.

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OS  HOMO SAPIENS (HUMAN).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC  PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE: 92154673.
RA  DALTON S., TREISMAN R.;
RT  "Characterization of SAP-1, a protein recruited by serum response
    factor to the c-fos serum response element.";
RL  CELL 68:597-612(1992).
RN  [2]
RP  REVISIONS.
RX  MEDLINE: 94123347.
RA  DALTON S., TREISMAN R.;
RT  "Characterization of SAP-1, a protein recruited by serum response
    factor to the c-fos serum response element.";
RL  CELL 76:411-411(1994).
CC  -1- FUNCTION: FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR
    (SRF). REQUIRES DNA-BOUND SRF FOR TERNARY COMPLEX FORMATION AND
    MAKES EXTENSIVE DNA CONTACTS TO THE 5' SIDE OF SRF, BUT DOES NOT
    BIND DNA AUTONOMOUSLY.
CC  -1- SUBCELLULAR LOCATION: NUCLEAR.
CC  -1- ALTERNATIVE PRODUCTS: TWO FORMS OF SAP-1 ARE PRODUCED BY
    ALTERNATIVE SPLICING OF THE SAME GENE, THEY ONLY DIFFER IN THE
    C-TERMINUS.
CC  -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC  -----
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CC  -----
CC  EMBL: M85165; G429186; -.
CC  DR  PIR: B42093; B42093.
CC  DR  MIM: 600246; -.
CC  DR  PROSITE: PS00345; ETS_DOMAIN_1; 1.
CC  DR  PROSITE: PS00346; ETS_DOMAIN_2; 1.
CC  DR  PROSITE: PS50061; ETS_DOMAIN_3; 1.
CC  DR  PFAM: PF00178; Ets; 1.
CC  DR  HSSP: P14921; 2STW.
CC  DR  TRANSFAC: T00737; -.
CC  KM  DNA-BINDING: NUCLEAR PROTEIN; ALTERNATIVE SPLICING.
CC  FT  DNA_BIND 5
CC  SQ  SEQUENCE 431 AA; 46827 MW; 2960052A CRC32;

Query Match          3.0%; Score 10; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  287 VARLMGIRKN 296
    |||||||
DB  41 VARLMGIRKN 50

RESULT  8
SAP1_MOUSE STANDARD: PRT; 430 AA.
AC  P41158;
DT  01-FEB-1995 (REL. 31, CREATED)
DT  01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT  01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE  SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (SAP-1A) (ETS-DOMAIN
DE  PROTEIN ELK-4).
DE  ELK4 OR SAP1.
OS  MUS MUSCULUS (MOUSE).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC  ROSENTIA; SCUROGNATHI; MORIDAE; MURINAE; MUS.
RN  [1]
RP  SEQUENCE FROM N.A.

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RC  TISSUE-EMBRYO;
RX  MEDLINE: 95047310.
RA  GIOVANE A., PINTZAS A., MAIRA S.-M., SOBIESZCZUK P., WASYLYK B.;
RT  "Net, a new ets transcription factor that is activated by Ras.";
RL  GENES DEV. 8:1502-1513(1994).
CC  -1- FUNCTION: CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
    FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
    ELEMENT.
CC  -1- SUBCELLULAR LOCATION: NUCLEAR.
CC  -1- TISSUE SPECIFICITY: LUNG AND LIVER.
CC  -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC  -----
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CC  -----
CC  EMBL: Z36885; G535128; -.
CC  DR  MGD: MGI:102853; ELK4.
CC  DR  PROSITE: PS00345; ETS_DOMAIN_1; 1.
CC  DR  PROSITE: PS00346; ETS_DOMAIN_2; 1.
CC  DR  PROSITE: PS50061; ETS_DOMAIN_3; 1.
CC  DR  PFAM: PF00178; Ets; 1.
CC  DR  HSSP: P14921; 2STW.
CC  KM  DNA-BINDING: NUCLEAR PROTEIN; ETS-DOMAIN.
CC  FT  DNA_BIND 5
CC  SQ  SEQUENCE 430 AA; 46867 MW; BE175C95 CRC32;

Query Match          3.0%; Score 10; DB 1; Length 430;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  287 VARLMGIRKN 296
    |||||||
DB  41 VARLMGIRKN 50

RESULT  9
SAP1_HUMAN STANDARD: PRT; 405 AA.
AC  P28323;
DT  01-DEC-1992 (REL. 24, CREATED)
DT  01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT  01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE  SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1B (SAP-1B) (ETS-DOMAIN
DE  PROTEIN ELK-4).
DE  ELK4 OR SAP1.
OS  HOMO SAPIENS (HUMAN).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC  PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE: 92154673.
RA  DALTON S., TREISMAN R.;
RT  "Characterization of SAP-1, a protein recruited by serum response
    factor to the c-fos serum response element.";
RL  CELL 68:597-612(1992).
CC  -1- FUNCTION: FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR
    (SRF). REQUIRES DNA-BOUND SRF FOR TERNARY COMPLEX FORMATION AND
    MAKES EXTENSIVE DNA CONTACTS TO THE 5' SIDE OF SRF, BUT DOES NOT
    BIND DNA AUTONOMOUSLY.
CC  -1- SUBCELLULAR LOCATION: NUCLEAR.
CC  -1- ALTERNATIVE PRODUCTS: TWO FORMS OF SAP-1 ARE PRODUCED BY
    ALTERNATIVE SPLICING OF THE SAME GENE, THEY ONLY DIFFER IN THE
    C-TERMINUS.
CC  -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC  -----
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 CC -----
 DR EMBL: M85164; G338035; -
 DR PIR: A42093; A42093.
 DR MIM: 600246; -
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PFAM: PF00178; Ets; 1.
 DR HSSP: P14921; 2STW.
 DR TRANSFAC: T02128; -
 DR DNA-BINDING: NUCLEAR PROTEIN; ALTERNATIVE SPLICING.
 FT DNA_BIND 5 85 ETS-DOMAIN.
 SQ SEQUENCE 405 AA: 44674 MW: C66EC15E CRC32;

Query Match 3.0%; Score 10; DB 1; Length 405;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 VARLWGIKRN 296
 |||||
 Db 41 VARLWGIKRN 50

RESULT 10
 DEVB_MYCLE STANDARD: PRT: 247 AA.
 AC 049700;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DE DEVB PROTEIN HOMOLOG.
 GN DEVB OR B1496_F1_31.
 OS MYCOBACTERIUM LEPRAE.
 CC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 CC ACTINOMYCETALES; CORYNEBACTERIINAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ROBISON K., SMITH D.R.;
 RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: PUTATIVE OXIDOREDUCTASE.
 CC -1- SIMILARITY: BELONGS TO THE SOL/DEVB FAMILY.
 CC -----
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 CC -----
 DR EMBL: U00013; G466869; -
 DR PFAM: PF01182; Glucosamine_iso; 1.
 DR OXIDOREDUCTASE.
 SQ SEQUENCE 247 AA: 26160 MW: DB677BF6 CRC32;

Query Match 2.4%; Score 8; DB 1; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 AAGAVGLE 39
 |||||
 Db 224 AAGAVGLE 231

RESULT 11
 ELK1_HUMAN

ID ELK1_HUMAN STANDARD: PRT: 428 AA.
 AC P19419;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DE ETS-DOMAIN PROTEIN ELK-1.
 GN ELK1.
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89203250.
 RA RAO V.N., HOEBNER K., ISOBE M., AR-RUSHDI A., CROCE C.M.,
 RA REDDY E.S.P.;
 RT "elk, tissue-specific ets-related genes on chromosomes X and 14 near
 RT translocation breakpoints."
 RL SCIENCE 244:66-70(1989).
 RN [2]
 RP DOMAINS.
 RX MEDLINE: 92334979.
 RA JANKNECHT R., NORDHEIM A.;
 RT "Elk-1 protein domains required for direct and SRF-assisted
 RT DNA-binding."
 RL NUCLEIC ACIDS RES. 20:3317-3324(1992).
 CC -1- FUNCTION: MAY STIMULATE TRANSCRIPTION. BINDS TO PURINE-RICH DNA
 CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
 CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
 CC ELEMENT.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: LUNG AND TESTIS.
 CC -1- PTM: PHOSPHORYLATED BY THE THREE GROUPS OF MAP KINASE (p38, JNK,
 CC AND ERK).
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: M25269; G538209; -
 DR PIR: A41354; TVHDEK.
 DR MIM: 311040; -
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PFAM: PF00178; Ets; 1.
 DR HSSP: P14921; 2STW.
 DR TRANSFAC: T00250; -
 DR NUCLEAR PROTEIN; DNA-BINDING; PHOSPHORYLATION.
 FT DNA_BIND 5 86 ETS-DOMAIN.
 SQ SEQUENCE 428 AA: 44915 MW: 4E43BDFF CRC32;

Query Match 2.4%; Score 8; DB 1; Length 428;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 MNVDRLSR 307
 |||||
 Db 55 MNVDRLSR 62

RESULT 12
 ELK1_MOUSE STANDARD: PRT: 429 AA.
 AC P41969;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE ETS-DOMAIN PROTEIN ELK-1.
 GN ELK1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC RODENTIA: SCIROGNATHI: MURIDAE: MURINAE: MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL: TISSUE-EMBRYO:
 RA GREVIN D., UNG S., DENHEZ F., DEHEM M., OUAATANNENS B., BEGUE A.,
 RA STEBELIN D., MARTIN P.;
 RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE OF 5-224 FROM N.A.
 RC TISSUE-EMBRYO:
 RX MEDLINE: 95047310.
 RA GIOVANE A., PINTZAS A., MAIRA S.-M., SOBIESZCZUK P., WASYLK B.;
 RT "Net, a new ets transcription factor that is activated by Ras.";
 RL GENES DEV. 8:1502-1513(1994).
 CC -1- FUNCTION: MAY STIMULATE TRANSCRIPTION. BINDS TO PURINE-RICH DNA
 CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
 CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
 CC ELEMENT.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND TO A
 CC LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: X87257; G836635; -;
 DR EMBL: Z36939; G535923; -;
 DR MGI: MGI:101833; ELK1.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PFAM: PF00178; ETS; 1.
 DR HSSP: P14921; 2STW.
 KW NUCLEAR PROTEIN; DNA-BINDING; PHOSPHORYLATION.
 FT DNA_BIND 5 86
 FT CONFLICT 133 133 P->T (IN REF. 2).
 FT SEQUENCE 429 AA: 45243 MW: F78E8069 CRC32;
 SQ
 Query Match 2.4%; Score 8; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 300 ANYDKLSR 307
 DB 55 ANYDKLSR 62
 RESULT 13
 ELK3_HUMAN STANDARD: PRT: 407 AA.
 ID ELK3_HUMAN
 AC P41970:
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN PROTEIN ELK-3 (ETS-RELATED PROTEIN NET) (SRF ACCESSORY
 DE PROTEIN 2) (SAP2).
 GN ELK3 OR NET.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE: 95047310.
 RA GIOVANE A., PINTZAS A., MAIRA S.-M., SOBIESZCZUK P., WASYLK B.;
 RT "Net, a new ets transcription factor that is activated by Ras.";
 RL GENES DEV. 8:1502-1513(1994).
 CC -1- FUNCTION: MAY BE A NEGATIVE REGULATOR OF TRANSCRIPTION BUT CAN
 CC ACTIVATE TRANSCRIPTION WHEN COEXPRESSED WITH RAS, SRC OR MOS.
 CC FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS
 CC AND SRF MOTIFS OF THE FOS SERUM RESPONSE ELEMENT.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: Z36715; G531523; -;
 DR MIM: 600247; -;
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PFAM: PF00178; ETS; 1.
 DR HSSP: P14921; 2STW.
 DR TRANSFAC: T01414; -;
 KW TRANSCRIPTION REGULATION; ACTIVATOR; REPRESSOR; NUCLEAR PROTEIN;
 KW DNA-BINDING.
 FT DNA_BIND 5 85
 FT CONFLICT 207 212 POLY-ALA.
 FT SEQUENCE 407 AA: 44365 MW: D0F7E21D CRC32;
 SQ
 Query Match 2.4%; Score 8; DB 1; Length 407;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 300 ANYDKLSR 307
 DB 54 ANYDKLSR 61
 RESULT 14
 ELK3_MOUSE STANDARD: PRT: 409 AA.
 ID ELK3_MOUSE
 AC P41971: P97747; Q62346;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN PROTEIN ELK-3 (ETS-RELATED PROTEIN NET) (ETS-RELATED
 DE PROTEIN ERP).
 GN ELK3 OR NET OR ERP.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 CC RODENTIA: SCIROGNATHI: MURIDAE: MURINAE: MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYO:
 RX MEDLINE: 95047310.
 RA GIOVANE A., PINTZAS A., MAIRA S.-M., SOBIESZCZUK P., WASYLK B.;
 RT "Net, a new ets transcription factor that is activated by Ras.";
 RL GENES DEV. 8:1502-1513(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C: TISSUE-LUNG;
 RX MEDLINE: 94217726.
 RA LOPEZ M., OERTGEN P., AKBARALI Y., DENDORFER U., LIBERMANN T.A.;
 RT "ERP, a new member of the ets transcription factor/oncoprotein
 RT family: cloning, characterization, and differential expression during
 RT B-lymphocyte development.";
 RL MOL. CELL. BIOL. 14:3292-3309(1994).
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 97047916.
 RA NOZAKI M., ONISHI Y., KANNO N., ONO Y., FUJIMURA Y.;
 RT Molecular cloning of Elk-3, a new member of the Ets family expressed
 RT during mouse embryogenesis and analysis of its transcriptional
 RT repression activity.
 RL DNA CELL BIOL. 15:855-862(1996).
 CC -1- FUNCTION: MAY BE A NEGATIVE REGULATOR OF TRANSCRIPTION BUT CAN
 CC ACTIVATE TRANSCRIPTION WHEN COEXRESSED WITH RAS, SRC OR MOS.
 CC FORMS A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS
 CC AND SRP MOTIFS OF THE FOS SERUM RESPONSE ELEMENT.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: HEART, LIVER, LUNG, KIDNEY AND MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC -----
 DR EMBL: Z32815; G479113; -
 DR EMBL: L19953; G436185; -
 DR EMBL: S82864; G1836130; -
 DR MGD: MG1:101762; ELK3.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PIRAM: PF00178; Ets; 1.
 DR HSSP: Q00422; IAWC.
 DR TRANSFAC: T01413; -
 DR KW TRANSCRIPTION REGULATION: ACTIVATOR; REPRESSOR; NUCLEAR PROTEIN;
 DR DNA-BINDING.
 KM DNA-BIND.
 FT DNA_BIND 5 85 ETS-DOMAIN.
 FT DOMAIN 208 212 POLY-ALA.
 FT CONFLICT 152 152 Q->E (IN REF. 1).
 FT CONFLICT 199 199 M->V (IN REF. 3).
 FT CONFLICT 238 238 A->V (IN REF. 1).
 FT CONFLICT 331 331 A->T (IN REF. 3).
 SQ SEQUENCE 409 AA: 44445 MW: 0PB56166 CRC32;
 Query Match 2.4%; Score 8; DB 1; Length 409;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 300 MNYDKLSR 307
 Db 54 MNYDKLSR 61
 RESULT 15
 ERF_HUMAN
 ID ERF_HUMAN STANDARD: PRT: 548 AA.
 AC P30548;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
 GN ERF.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96030784.
 RA SCOURAS D.N., ATHANASSIOU M.A., BEAL G.J. JR., FISHER R.J., BLAIR D.G.,
 RA MAYROTHALASSITIS G.J.;
 RT "ERF: an Ets domain protein with strong transcriptional repressor
 RT activity, can suppress ets-associated tumorigenesis and is regulated
 RT by phosphorylation during cell cycle and mitogenic stimulation.";

RL EMBL J. 14:4781-4793(1995).
 CC -1- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE A1
 CC ELEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED
 CC IN CELLULAR PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- PMW: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 DR EMBL: U15655; G1015337; -
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR PIRAM: PF00178; Ets; 1.
 DR HSSP: Q01543; IFLI.
 DR KW TRANSCRIPTION REGULATION: REPRESSOR; DNA-BINDING; NUCLEAR PROTEIN;
 DR PHOSPHORYLATION.
 KM DNA_BIND 27 107 ETS-DOMAIN.
 FT DOMAIN 166 171 POLY-SER.
 FT DOMAIN 290 293 POLY-GLY.
 FT DOMAIN 362 373 POLY-SER.
 FT DOMAIN 418 423 POLY-PRO.
 FT DOMAIN 496 499 POLY-GLY.
 FT MOD_RES 526 526 PHOSPHORYLATION (BY ERK2).
 FT MUTAGEN 526 526 T->A: LOSS OF A PHOSPHORYLATION SITE.
 SQ SEQUENCE 548 AA: 58776 MW: 971D7F6D CRC32;
 Query Match 2.4%; Score 8; DB 1; Length 548;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 300 MNYDKLSR 307
 Db 76 MNYDKLSR 83

Search completed: November 20, 1999, 18:05:36
 Job time: 313 sec